IN THE CLAIMS:

1-87. (cancelled)

88. (new) A method of identifying one or more etiologic agents of disease in a sample comprising the steps of:

amplifying two or more segments of a nucleic acid from said one or more etiologic agents in said sample with two or more primer pairs to obtain two or more amplification products;

determining two or more base compositions of said two or more amplification products; and

comparing said two or more base compositions with known base compositions of known etiologic agents produced with said two or more primer pairs to identify said one or more etiologic agents in said sample.

89 (new) The method of claim 88, wherein said determining two or more base compositions of said two or more amplification products is conducted without sequencing.

90. (new) The method of claim 88, wherein the amplification products are double-stranded and the base compositions are determined for both strands of the double-stranded amplification products.

91. (new) The method of claim 88, wherein identification of said one or more etiologic agents is accomplished at the genus level.

92. (new) The method of claim 88, wherein said base compositions of said amplification products are calculated from molecular masses determined by mass spectrometry.

93. (new) The method of claim 92, wherein said mass spectrometry is Fourier transform ion cyclotron resonance mass spectrometry (FTICR- MS), ion trap mass spectrometry, quadrupole mass spectrometry, magnetic sector mass spectrometry, time of flight (TOF) mass spectrometry, Q-TOF mass spectrometry, or triple quadrupole mass spectrometry.

94. (new) The method of claim 88, wherein said one or more etiologic agents comprise a bacterium, a virus, a protozoan, a parasite, a mold, a fungus, or any combination thereof.

95. (new) The method of claim 88, wherein said sample is a biological sample selected from the group consisting of blood, mucus, hair, urine, breath, sputum, saliva, stool, nail, and tissue.

96. (new) The method of claim 88, wherein said sample is obtained from a human.

97. (new) The method of claim 88, wherein said two or more primer pairs hybridize to nucleic acid encoding ribosomal RNA.

98. (new) The method of claim 88, wherein said two or more segments of nucleic acid are from ribosomal RNA and at least one gene encoding a protein that participates in translation, replication, recombination, repair, transcription, nucleotide metabolism, amino acid metabolism, lipid metabolism, uptake, secretion, antibiotic resistance, virulence, or pathogenicity.

99. (new) The method of claim 88, wherein said one or more etiologic agents are previously unknown etiologic agents.

100. (new) The method of claim 88, wherein said two or more segments of a nucleic acid are amplified from a single gene.

101. (new) The method of claim 88, wherein said two or more segments of a nucleic acid are amplified from different genes.

102. (new) The method of claim 88, wherein the two or more segments of nucleic acid are from two or more different etiologic agents.

103. (new) The method of claim 102, wherein each of said two or more different etiologic are selected from the group consisting of: a bacterium, a virus, a protozoan, a parasite, a mold, and a fungus.

104. (new) The method of claim 103, wherein a first of said two or more different etiologic agents is from one member of said group and a second of said two or more different etiologic agents is from a different member of said group.

105. (new) The method of claim 88, wherein the two or more segments of nucleic acid are from three or more different etiologic agents.

106. (new) The method of claim 88, wherein said one or more etiologic agents of disease comprise a bacterium.

107. (new) The method of claim 88, wherein said one or more etiologic agents of disease comprise two or more different bacteria.

108. (new) The method of claim 107, wherein said two or more different bacteria are from two different genera.

109. (new) The method of claim 108, wherein said two different genera are selected from the group consisting of *Acinetobacter*, *Aeromonas*, *Bacillus*, *Bacteriodes*, *Bartonella*, *Bordetella*, *Borrelia*, *Brucella*, *Burkholderia*, *Campylobacter*, *Chlamydia*,

Chlamydophila, *Clostridium*, *Coxiella*, *Enterococcus*, *Escherichia*, *Francisella*, *Fusobacterium*, *Haemophilus*, *Helicobacter*, *Klebsiella*, *Legionella*, *Leptospira*, *Listeria*, *Moraxella*, *Mycobacterium*, *Mycoplasma*, *Neisseria*, *Proteus*, *Pseudomonas*, *Rhodobacter*, *Rickettsia*, *Salmonella*, *Shigella*, *Staphylococcus*, *Streptobacillus*, *Streptomyces*, *Treponema*, *Ureaplasma*, *Vibrio*, and *Yersinia*.

110. (new) The method of claim 107, wherein said two or more different bacteria are from two different species.

111. (new) The method of claim 107, wherein said two or more different bacteria are two different subspecies.

112. (new) The method of claim 88, wherein said one or more etiologic agents of disease comprise at least one bacterium and at least one virus.

113. (new) The method of claim 88, wherein said one or more etiologic agents of disease comprise two different viruses.

114. (new) The method of claim 113, wherein said two or more different viruses are from two different viral families.

115. (new) The method of claim 114, wherein said two different viral families are selected from the group consisting of *Filoviridae, Flaviviridae, Arenaviridae, Bunyaviridae, Adenoviridae, Picornaviridae, Togaviridae,* and *Coronaviridae.*

116. (new) The method of claim 113, wherein said two or more different viruses are from two different species.

117. (new) The method of claim 113, wherein said two or more different viruses are two different subspecies.

118. (new) The method of claim 88, wherein said two or more segments of nucleic acid are from two or genes selected from the group consisting of: 16S rRNA, 23S rRNA, infB, rpoC, tufB, rplB, rpoB, valS, dnaK, hflB, groL, hexon, RNaseP, cya, aspS, gki, gtr, murI, mutS, xpt, ygiL, DdDp, DdRpA, and DdRpB.

119. (new) A method of identifying one or more bioagents in a sample comprising the steps of:

amplifying two or more segments of a nucleic acid from said one or more of bioagents in said sample with two or more primer pairs to obtain two or more amplification products;

determining two or more base compositions of said two or more amplification products; and

comparing said two or more base compositions with known base compositions of known bioagents produced with said two or more primer pairs to identify said one or more bioagents in said sample.

120. (new) The method of claim 119, wherein said determining two or more base compositions of said two or more amplification products is conducted without sequencing.

121. (new) The method of claim 119, wherein the amplification products are double-stranded and the base compositions are determined for both strands of the double-stranded amplification products.

122. (new) A method of claim 119, wherein said two or more base compositions are calculated from masses of said two or more amplification products.

123. (new) The method of claim 122, wherein the masses of the two or more amplification products are obtained via mass spectrometry.

124. (new) The method of claim 119, wherein said one or more bioagents in said sample cannot be identified using a single primer pair of said two or more primer pairs.

125. (new) The method of claim 119, wherein said one or more bioagents in a sample are identified by comparing three or more base compositions to a database of bioagents produced with three or more primer pairs.

126. (new) The method of claim 119, wherein said two or more segments of a nucleic acid are amplified from a single gene.

127. (new) The method of claim 119, wherein said two or more segments of a nucleic acid are amplified from different genes.

128. (new) The method of claim 119, wherein said one or more bioagents is an organism.

129. (new) The method of claim 128, wherein said organism is a human, a protozoan, a bacterium, a virus, a parasite, a mold, or a fungus

130. (new) The method of claim 119, wherein the two or more segments of nucleic acid are from two or more different bioagents.

131. (new) The method of claim 130, wherein each of said two or more different bioagents are selected from the group consisting of: a human, a bacterium, a virus, a protozoan, a parasite, a mold, and a fungus.

132. (new) The method of claim 131, wherein a first of said two or more different bioagents is from one member of said group and a second of said two or more different bioagents is from a different member of said group.

133. (new) The method of claim 119, wherein the two or more segments of nucleic acid are from three or more different bioagents.

134. (new) The method of claim 119, wherein said one or more biogents comprise a bacterium.

135. (new) The method of claim 119, wherein said one or more bioagents comprise two or more different bacteria.

136. (new) The method of claim 135, wherein said two or more different bacteria are from two different genera.

137. (new) The method of claim 136, wherein said two different genera are selected from the group consisting of *Acinetobacter*, *Aeromonas*, *Bacillus*, *Bacteriodes*, *Bartonella*, *Bordetella*, *Borrelia*, *Brucella*, *Burkholderia*, *Campylobacter*, *Chlamydia*, *Chlamydophila*, *Clostridium*, *Coxiella*, *Enterococcus*, *Escherichia*, *Francisella*, *Fusobacterium*, *Haemophilus*, *Helicobacter*, *Klebsiella*, *Legionella*, *Leptospira*, *Listeria*, *Moraxella*, *Mycobacterium*, *Mycoplasma*, *Neisseria*, *Proteus*, *Pseudomonas*, *Rhodobacter*, *Rickettsia*, *Salmonella*, *Shigella*, *Staphylococcus*, *Streptobacillus*, *Streptomyces*, *Treponema*, *Ureaplasma*, *Vibrio*, and *Yersinia*.

138. (new) The method of claim 135, wherein said two or more different bacteria are from two different species.

139. (new) The method of claim 135, wherein said two or more different bacteria are two different subspecies.

140. (new) The method of claim 119, wherein said one or more bioagents comprise at least one bacterium and at least one virus.

141. (new) The method of claim 119, wherein said one or more bioagents comprise two different viruses.

142. (new) The method of claim 139, wherein said two or more different viruses are from two different viral families.

143. (new) The method of claim 142, wherein said two different viral families are selected from the group consisting of *Filoviridae, Flaviviridae, Arenaviridae, Bunyaviridae, Adenoviridae, Picornaviridae, Togaviridae,* and *Coronaviridae.*

144. (new) The method of claim 141, wherein said two or more different viruses are from two different species.

145. (new) The method of claim 141, wherein said two or more different viruses are two different subspecies.

146. (new) The method of claim 119, wherein said two or more segments of nucleic acid are from two or genes selected from the group consisting of: 16S rRNA, 23S rRNA, infB, rpoC, tufB, rplB, rpoB, valS, dnaK, hflB, groL, hexon, RNaseP, cya, aspS, gki, gtr, murI, mutS, xpt, ygiL, DdDp, DdRpA, and DdRpB.

147. (new) A method of identifying one or more bioagents in a sample comprising the steps of:

amplifying two or more segments of a nucleic acid from said one or more of bioagents in said sample with two or more primer pairs to obtain two or more amplification products, wherein each of the primer pairs hybridizes to conserved regions of the nucleic acid that flank a variable region;

determining two or more base compositions of said two or more amplification products; and

comparing said two or more base compositions with a database containing known base compositions of known bioagents produced with said two or more primer pairs to identify said one or more bioagents in said sample.

148. (new) The method of claim 147, wherein said determining two or more base compositions of said two or more amplification products is conducted without sequencing.

149. (new) The method of claim 147, wherein the amplification products are double-stranded and the base compositions are determined for both strands of the double-stranded amplification products.

150. (new) The method of claim 147, wherein said variable region varies between at least two or said bioagents.

151. (new) The method of claim 147, wherein said variable region uniquely varies between at least five of said bioagents.

152. (new) The method of claim 147, wherein said variable region uniquely varies between at least nineteen of said bioagents.

153. (new) The method of claim 147, wherein said two or more base compositions are calculated from masses of said two or more amplification products.

154. (new) The method of claim 153, wherein the masses of the two or more amplification products are obtained via mass spectrometry.

155. (new) The method of claim 147, wherein said one or more bioagents in said sample cannot be identified using a single primer pair of said two or more primer pairs.

156. (new) The method of claim 147, wherein said one or more bioagents in a sample are identified by comparing three or more base compositions to a database of bioagents produced with three or more primer pairs.

157. (new) The method of claim 147, wherein said two or more segments of a nucleic acid are amplified from a single gene.

158. (new) The method of claim 147, wherein said two or more segments of a nucleic acid are amplified from different genes.

159. (new) The method of claim 147, wherein said one or more bioagents is an organism.

160. (new) The method of claim 159, wherein said organism is a human, a protozoan, a bacterium, a virus, a parasite, a mold, or a fungus.

161. (new) The method of claim 147, wherein the two or more segments of nucleic acid are from two or more different bioagents.

162. (new) The method of claim 161, wherein each of said two or more different bioagents are selected from the group consisting of: a human, a bacterium, a virus, a protozoan, a parasite, a mold, and a fungus.

163. (new) The method of claim 162, wherein a first of said two or more different bioagents is from one member of said group and a second of said two or more different bioagents is from a different member of said group.

164. (new) The method of claim 147, wherein the two or more segments of nucleic acid are from three or more different bioagents.

165. (new) The method of claim 147, wherein said one or more biogents comprise a bacterium.

166. (new) The method of claim 147, wherein said one or more bioagents comprise two or more different bacteria.

167. (new) The method of claim 166, wherein said two or more different bacteria are from two different genera.

168. (new) The method of claim 167, wherein said two different genera are selected from the group consisting of *Acinetobacter*, *Aeromonas*, *Bacillus*, *Bacteriodes*, *Bartonella*, *Bordetella*, *Borrelia*, *Brucella*, *Burkholderia*, *Campylobacter*, *Chlamydia*, *Chlamydophila*, *Clostridium*, *Coxiella*, *Enterococcus*, *Escherichia*, *Francisella*, *Fusobacterium*, *Haemophilus*, *Helicobacter*, *Klebsiella*, *Legionella*, *Leptospira*, *Listeria*, *Moraxella*, *Mycobacterium*, *Mycoplasma*, *Neisseria*, *Proteus*, *Pseudomonas*, *Rhodobacter*, *Rickettsia*, *Salmonella*, *Shigella*, *Staphylococcus*, *Streptobacillus*, *Streptomyces*, *Treponema*, *Ureaplasma*, *Vibrio*, and *Yersinia*.

169. (new) The method of claim 166, wherein said two or more different bacteria are from two different species.

170. (new) The method of claim 166, wherein said two or more different bacteria are two different subspecies.

171. (new) The method of claim 147, wherein said one or more bioagents comprise at least one bacterium and at least one virus.

172. (new) The method of claim 147, wherein said one or more bioagents comprise two different viruses.

173. (new) The method of claim 172, wherein said two or more different viruses are from two different viral families.

174. (new) The method of claim 173, wherein said two different viral families are selected from the group consisting of *Filoviridae, Flaviviridae, Arenaviridae, Bunyaviridae, Adenoviridae, Picornaviridae, Togaviridae,* and *Coronaviridae.*

175. (new) The method of claim 172, wherein said two or more different viruses are from two different species.

176. (new) The method of claim 172, wherein said two or more different viruses are two different subspecies.

177. (new) The method of claim 147, wherein said two or more segments of nucleic acid are from two or genes selected from the group consisting of: 16S rRNA, 23S rRNA, infB, rpoC, tufB, rplB, rpoB, valS, dnaK, hflB, groL, hexon, RNaseP, cya, aspS, gki, gtr, murI, mutS, xpt, ygiL, DdDp, DdRpA, and DdRpB.

178. (new) A method of identifying one or more bioagents in a sample comprising the steps of:

amplifying two or more segments of a nucleic acid from said one or more of bioagents in said sample with two or more primer pairs to obtain two or more amplification products, wherein each of the primer pairs hybridizes to conserved regions of the nucleic acid that flank a variable region;

determining the mass of said two or more amplification products via mass spectrometry, without sequencing; and

comparing said masses with a database containing known masses of known bioagents produced with said two or more primer pairs to identify said one or more bioagents in said sample.

179. (new) The method of claim 178, further comprising the step of calculating base compositions of said two or more amplification products, using said determined masses.

180. (new) The method of claim 178, wherein the amplification products are double-stranded and mass is determined for both strands of the double-stranded amplification products.

181. (new) The method of claim 178, wherein said variable region varies between at least two or said bioagents.

182. (new) The method of claim 178, wherein said variable region uniquely varies between at least five of said bioagents.

183. (new) The method of claim 178, wherein said variable region uniquely varies between at least nineteen of said bioagents.

184. (new) The method of claim 178, wherein said one or more bioagents in said sample cannot be identified using a single primer pair of said two or more primer pairs.

185. (new) The method of claim 178, wherein said one or more bioagents in a sample are identified by comparing three or more masses to a database of bioagents produced with three or more primer pairs.

186. (new) The method of claim 178, wherein said two or more segments of a nucleic acid are amplified from a single gene.

187. (new) The method of claim 178, wherein said two or more segments of a nucleic acid are amplified from different genes.

188. (new) The method of claim 178, wherein said one or more bioagents is an organism.

189. (new) The method of claim 188, wherein said organism is a human, a protozoan, a bacterium, a virus, a parasite, a mold, or a fungus.

190. (new) The method of claim 178, wherein the two or more segments of nucleic acid are from two or more different bioagents.

191. (new) The method of claim 190, wherein each of said two or more different bioagents are selected from the group consisting of: a human, a bacterium, a virus, a protozoan, a parasite, a mold, and a fungus.

192. (new) The method of claim 191, wherein a first of said two or more different bioagents is from one member of said group and a second of said two or more different bioagents is from a different member of said group.

193. (new) The method of claim 178, wherein the two or more segments of nucleic acid are from three or more different bioagents.

194. (new) The method of claim 178, wherein said one or more biogents comprise a bacterium.

195. (new) The method of claim 178, wherein said one or more bioagents comprise two or more different bacteria.

196. (new) The method of claim 195, wherein said two or more different bacteria are from two different genera.

197. (new) The method of claim 196, wherein said two different genera are selected from the group consisting of *Acinetobacter*, *Aeromonas*, *Bacillus*, *Bacteriodes*, *Bartonella*, *Bordetella*, *Borrelia*, *Brucella*, *Burkholderia*, *Campylobacter*, *Chlamydia*, *Chlamydophila*, *Clostridium*, *Coxiella*, *Enterococcus*, *Escherichia*, *Francisella*, *Fusobacterium*, *Haemophilus*, *Helicobacter*, *Klebsiella*, *Legionella*, *Leptospira*, *Listeria*, *Moraxella*, *Mycobacterium*, *Mycoplasma*, *Neisseria*, *Proteus*, *Pseudomonas*, *Rhodobacter*, *Rickettsia*, *Salmonella*, *Shigella*, *Staphylococcus*, *Streptobacillus*, *Streptomyces*, *Treponema*, *Ureaplasma*, *Vibrio*, and *Yersinia*.

198. (new) The method of claim 195, wherein said two or more different bacteria are from two different species.

199. (new) The method of claim 195, wherein said two or more different bacteria are two different subspecies.

200. (new) The method of claim 178, wherein said one or more bioagents comprise at least one bacterium and at least one virus.

201. (new) The method of claim 178, wherein said one or more bioagents comprise two different viruses.

202. (new) The method of claim 201, wherein said two or more different viruses are from two different viral families.

203. (new) The method of claim 202, wherein said two different viral families are selected from the group consisting of *Filoviridae, Flaviviridae, Arenaviridae, Bunyaviridae, Adenoviridae, Picornaviridae, Togaviridae,* and *Coronaviridae.*

204. (new) The method of claim 201, wherein said two or more different viruses are from two different species.

205. (new) The method of claim 201, wherein said two or more different viruses are two different subspecies.

206. (new) The method of claim 178, wherein said two or more segments of nucleic acid are from two or genes selected from the group consisting of: 16S rRNA, 23S rRNA, infB, rpoC, tufB, rplB, rpoB, valS, dnaK, hflB, groL, hexon, RNaseP, cya, aspS, gki, gtr, murI, mutS, xpt, ygiL, DdDp, DdRpA, and DdRpB.